

# Errors Corrected by the STIC Systems Branch

Serial Number: 09/998,080

CRF Processing Date: 11/29/01

Edited by: DC

Verified by: DC (STIC sta

**ENTERED**

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☒ Other: Corrected obvious mistakes (2) in numbering of amino acid.

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/990,080

DATE: 12/03/2001  
 TIME: 09:26:41

Input Set : A:\PTO.DC.txt  
 Output Set: N:\CRF3\12032001\I990080.raw

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3 <110> APPLICANT: Morin, Gregg B.
4   Geron Corporation
6 <120> TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
8 <130> FILE REFERENCE: 018/258c
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/990,080
C--> 11 <141> CURRENT FILING DATE: 1998-08-03
W--> 13 <140> CURRENT APPLICATION NUMBER: US 09/128,354
C--> 14 <141> CURRENT FILING DATE: 1998-08-03
16 <150> PRIOR APPLICATION NUMBER: US 09/052,864
17 <151> PRIOR FILING DATE: 1998-03-31
19 <160> NUMBER OF SEQ ID NOS: 21
21 <170> SOFTWARE: PatentIn Ver. 2.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 4015
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (56)..(3454)
31 <223> OTHER INFORMATION: human telomerase reverse transcriptase (hTERT) cDNA
33 <400> SEQUENCE: 1
34 gcagcgtgc gtcctgctgc gcacgtggga agccctggcc ccggccaccc ccgcg atg 58
35                                     Met
36                                     1
38 ccg cgc gct ccc cgc tgc cga gcc gtg cgc tcc ctg ctg cgc agc cac 106
39 Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His
40           5           10           15
42 tac cgc gag gtg ctg ccg ctg gcc acg ttc gtg cgg cgc ctg ggg ccc 154
43 Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro
44           20           25           30
46 cag ggc tgg cgg ctg gtg cag cgc ggg gac ccg gcg gct ttc cgc gcg 202
47 Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala
48           35           40           45
50 ctg gtg gcc cag tgc ctg gtg tgc gtg ccc tgg gac gca cgg ccg ccc 250
51 Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro
52 50           55           60           65
54 ccc gcc gcc ccc tcc ttc cgc cag gtg tcc tgc ctg aag gag ctg gtg 298
55 Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val
56           70           75           80
58 gcc cga gtg ctg cag agg ctg tgc gag cgc ggc gcg aag aac gtg ctg 346
59 Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu
60           85           90           95
62 gcc ttc ggc ttc gcg ctg ctg gac ggg gcc cgc ggg ggc ccc ccc gag 394
63 Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu
64           100          105          110
66 gcc ttc acc acc agc gtg cgc agc tac ctg ccc aac acg gtg acc gac 442
67 Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp

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Input Set : A:\PTO.DC.txt

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71	Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg Arg Val Gly			
72	130 135 140 145			
74	gac gac gtg ctg gtt cac ctg ctg gca cgc tgc gcg ctc ttt gtg ctg	538		
75	Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu			
76	150 155 160			
78	gtg gct ccc agc tgc gcc tac cag gtg tgc ggg ccg ccg ctg tac cag	586		
79	Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln			
80	165 170 175			
82	ctc ggc gct gcc act cag gcc ccg ccc cca cac gct agt gga ccc	634		
83	Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro			
84	180 185 190			
86	cga agg cgt ctg gga tgc gaa cgg gcc tgg aac cat agc gtc agg gag	682		
87	Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu			
88	195 200 205			
90	gcc ggg gtc ccc ctg ggc ctg cca gcc ccg ggt gcg agg agg cgc ggg	730		
91	Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly			
92	210 215 220 225			
94	ggc agt gcc agc cga agt ctg ccg ttg ccc aag agg ccc agg cgt gcc	778		
95	Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly			
96	230 235 240			
98	gct gcc cct gag ccg gag cgg acg ccc gtt ggg cag ggg tcc tgg gcc	826		
99	Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala			
100	245 250 255			
102	cac ccg ggc agg acg cgt gga ccg agt gac cgt ggt ttc tgt gtg gtg	874		
103	His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val			
104	260 265 270			
106	tca cct gcc aga ccc gcc gaa gaa gcc acc tct ttg gag ggt gcg ctc	922		
107	Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu			
108	275 280 285			
110	tct ggc acg cgc cac tcc cac cca tcc gtg ggc cgc cag cac cac gcg	970		
111	Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala			
112	290 295 300 305			
114	ggc ccc cca tcc aca tgc cgg cca cca cgt ccc tgg gac acg cct tgt	1018		
115	Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys			
116	310 315 320			
118	ccc ccg gtg tac gcc gag acc aag cac ttc ctc tac tcc tca ggc gac	1066		
119	Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp			
120	325 330 335			
122	aag gag cag ctg cgg ccc tcc ttc cta ctc agc tct ctg agg ccc agc	1114		
123	Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser			
124	340 345 350			
126	ctg act ggc gct cgg agg ctc gtg gag acc atc ttt ctg ggt tcc agg	1162		
127	Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg			
128	355 360 365			
130	ccc tgg atg cca ggg act ccc cgc agg ttg ccc cgc ctg ccc cag cgc	1210		
131	Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg			
132	370 375 380 385			

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135	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	Asn	His	Ala	
136					390					395				400			
138	cag	tgc	ccc	tac	ggg	gtg	ctc	ctc	aag	acg	cac	tgc	ccg	ctg	cga	gct	1306
139	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	Leu	Arg	Ala	
140				405					410					415			
142	gcg	gtc	acc	cca	gca	gcc	ggt	gtc	tgt	gcc	cgg	gag	aag	ccc	cag	ggc	1354
143	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	Pro	Gln	Gly	
144			420					425						430			
146	tct	gtg	gcg	gcc	ccc	gag	gag	gag	gac	aca	gac	ccc	cgt	cgc	ctg	gtg	1402
147	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	Arg	Leu	Val	
148			435					440					445				
150	cag	ctg	ctc	cgc	cag	cac	agc	agc	ccc	tgg	cag	gtg	tac	ggc	ttc	gtg	1450
151	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	Gly	Phe	Val	
152	450				455						460				465		
154	cgg	gcc	tgc	ctg	cgc	cgg	ctg	gtg	ccc	cca	ggc	ctc	tgg	ggc	tcc	agg	1498
155	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	Gly	Ser	Arg	
156				470					475					480			
158	cac	aac	gaa	cgc	ctc	ttc	ctc	agg	aac	acc	aag	aag	ttc	atc	tcc	ctg	1546
159	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser	Leu	
160				485					490					495			
162	ggg	aag	cat	gcc	aag	ctc	tcg	ctg	cag	gag	ctg	acg	tgg	aag	atg	agc	1594
163	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	Lys	Met	Ser	
164			500					505						510			
166	gtg	cgg	gac	tgc	gct	tgg	ctg	cgc	agg	agc	cca	ggg	gtt	ggc	tgt	gtt	1642
167	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys	Val	
168			515				520						525				
170	ccg	gcc	gca	gag	cac	cgt	ctg	cgt	gag	gag	atc	ctg	gcc	aag	ttc	ctg	1690
171	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe	Leu	
172	530				535						540				545		
174	cac	tgg	ctg	atg	agt	gtg	tac	gtc	gtc	gag	ctg	ctc	agg	tct	ttc	ttt	1738
175	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	
176				550					555					560			
178	tat	gtc	acg	gag	acc	acg	ttt	caa	aag	aac	agg	ctc	ttt	ttc	tac	cgg	1786
179	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	Arg	
180				565					570					575			
182	aag	agt	gtc	tgg	agc	aag	ttg	caa	agc	att	gga	atc	aga	cag	cac	ttg	1834
183	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His	Leu	
184			580					585						590			
186	aag	agg	gtg	cag	ctg	cgg	gag	ctg	tcg	gaa	gca	gag	gtc	agg	cag	cat	1882
187	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln	His	
188			595				600						605				
190	cgg	gaa	gcc	agg	ccc	gcc	ctg	ctg	acg	tcc	aga	ctc	cgc	ttc	atc	ccc	1930
191	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile	Pro	
192	610				615						620				625		
194	aag	cct	gac	ggg	ctg	cgg	ccg	att	gtg	aac	atg	gac	tac	gtc	gtg	gga	1978
195	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr	Val	Val	Gly	
196				630						635				640			
198	gcc	aga	acg	ttc	cgc	aga	gaa	aag	agg	gcc	gag	cgt	ctc	acc	tcg	agg	2026

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199	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu	Thr	Ser	Arg	
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202	gtg	aag	gca	ctg	ttc	agc	gtg	ctc	aac	tac	gag	cgg	gcg	cgg	cgc	ccc	2074
203	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala	Arg	Arg	Pro	
204			660					665					670				
206	ggc	ctc	ctg	ggc	gcc	tct	gtg	ctg	ggc	ctg	gac	gat	atc	cac	agg	gcc	2122
207	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile	His	Arg	Ala	
208		675						680					685				
210	tgg	cgc	acc	ttc	gtg	ctg	cgt	gtg	cgg	gcc	cag	gac	ccg	ccg	cct	gag	2170
211	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro	Pro	Pro	Glu	
212	690					695				700						705	
214	ctg	tac	ttt	gtc	aag	gtg	gat	gtg	acg	ggc	gcg	tac	gac	acc	atc	ccc	2218
215	Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp	Thr	Ile	Pro	
216				710						715					720		
218	cag	gac	agg	ctc	acg	gag	gtc	atc	gcc	agc	atc	atc	aaa	ccc	cag	aac	2266
219	Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys	Pro	Gln	Asn	
220			725						730					735			
222	acg	tac	tgc	gtg	cgt	cgg	tat	gcc	gtg	gtc	cag	aag	gcc	gcc	cat	ggg	2314
223	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala	Ala	His	Gly	
224			740					745					750				
226	cac	gtc	cgc	aag	gcc	ttc	aag	agc	cac	gtc	tct	acc	ttg	aca	gac	ctc	2362
227	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser	Thr	Leu	Thr	Asp	Leu	
228		755					760					765					
230	cag	ccg	tac	atg	cga	cag	ttc	gtg	gct	cac	ctg	cag	gag	acc	agc	ccg	2410
231	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	Glu	Thr	Ser	Pro	
232	770					775					780				785		
234	ctg	agg	gat	gcc	gtc	gtc	atc	gag	cag	agc	tcc	tcc	ctg	aat	gag	gcc	2458
235	Leu	Arg	Asp	Ala	Val	Ile	Glu	Gln	Ser	Ser	Ser	Ser	Leu	Asn	Glu	Ala	
236				790					795					800			
238	agc	agt	ggc	ctc	ttc	gac	gtc	ttc	cta	cgc	ttc	atg	tgc	cac	cac	gcc	2506
239	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe	Met	Cys	His	His	Ala	
240			805						810					815			
242	gtg	cgc	atc	agg	ggc	aag	tcc	tac	gtc	cag	tgc	cag	ggg	atc	ccg	cag	2554
243	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys	Gln	Gly	Ile	Pro	Gln	
244			820					825					830				
246	ggc	tcc	atc	ctc	tcc	acg	ctg	ctc	tgc	agc	ctg	tgc	tac	ggc	gac	atg	2602
247	Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly	Asp	Met	
248		835					840					845					
250	gag	aac	aag	ctg	ttt	gcg	ggg	att	cgg	cgg	gac	ggg	ctg	ctc	ctg	cgt	2650
251	Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp	Gly	Leu	Leu	Leu	Arg	
252	850					855					860				865		
254	ttg	gtg	gat	gat	ttc	ttg	ttg	gtg	aca	cct	cac	ctc	acc	cac	gcg	aaa	2698
255	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr	His	Ala	Lys	
256					870					875					880		
258	acc	ttc	ctc	agg	acc	ctg	gtc	cga	ggg	gtc	cct	gag	tat	ggc	tgc	gtg	2746
259	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly	Cys	Val	
260			885						890						895		
262	gtg	aac	ttg	cgg	aag	aca	gtg	gtg	aac	ttc	cct	gta	gaa	gac	gag	gcc	2794
263	Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro	Val	Glu	Asp	Glu	Ala	

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266	ctg ggt ggc acg gct ttt gtt cag atg ccg gcc cac ggc cta ttc ccc	2842		
267	Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro			
268	915	920	925	
270	tgg tgc ggc ctg ctg ctg gat acc cgg acc ctg gag gtg cag agc gac	2890		
271	Trp Cys Gly Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp			
272	930	935	940	945
274	tac tcc agc tat gcc cgg acc tcc atc aga gcc agt ctc acc ttc aac	2938		
275	Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn			
276	950	955	960	
278	cgc ggc ttc aag gct ggg agg aac atg cgt cgc aaa ctc ttt ggg gtc	2986		
279	Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val			
280	965	970	975	
282	ttg cgg ctg aag tgt cac agc ctg ttt ctg gat ttg cag gtg aac agc	3034		
283	Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser			
284	980	985	990	
286	ctc cag acg gtg tgc acc aac atc tac aag atc ctc ctg ctg cag gcg	3082		
287	Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala			
288	995	1000	1005	
290	tac agg ttt cac gca tgt gtg ctg cag ctc cca ttt cat cag caa gtt	3130		
291	Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val			
292	1010	1015	1020	1025
294	tgg aag aac ccc aca ttt ttc ctg cgc gtc atc tct gac acg gcc tcc	3178		
295	Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser			
296	1030	1035	1040	
298	ctc tgc tac tcc atc ctg aaa gcc aag aac gca ggg atg tgc ctg ggg	3226		
299	Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly			
300	1045	1050	1055	
302	gcc aag ggc gcc gcc ggc cct ctg ccc tcc gag gcc gtg cag tgg ctg	3274		
303	Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu			
304	1060	1065	1070	
306	tgc cac caa gca ttc ctg ctc aag ctg act cga cac cgt gtc acc tac	3322		
307	Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr			
308	1075	1080	1085	
310	gtg cca ctc ctg ggg tca ctc agg aca gcc cag acg cag ctg agt cgg	3370		
311	Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg			
312	1090	1095	1100	1105
314	aag ctc ccg ggg acg acg ctg act gcc ctg gag gcc gca gcc aac ccg	3418		
315	Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro			
316	1110	1115	1120	
318	gca ctg ccc tca gac ttc aag acc atc ctg gac tga tggccacccg	3464		
319	Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp			
320	1125	1130		
322	cccacagcca ggccgagagc agacaccagc agccctgtca cgccgggctc tacgtcccag	3524		
324	ggagggaggg gcgggccaca ccagggcccg caccgctggg agtctgaggg ctgagtgagt	3584		
326	gtttggccga ggccctgcatg tccgctgaa ggctgagtgt ccggctgagg cctgagcgag	3644		
328	tgtccagcca agggctgagt gtccagcaca cctgcccgtct tcacttcccc acaggctggc	3704		
330	gctcggctcc accccagggc cagcttttcc tcaccaggag ccgggcttcc actccccaca	3764		
332	taggaatagt ccatccccag attcgccatt gttcaccctt cgccctgccc tcctttgcct	3824		

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:13 M:280 W: Numeric Identifier already exists, <140> found multiple times  
L:13 M:281 W: Numeric Fields not Ordered, <140> not ordered!.  
L:13 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:14 M:280 W: Numeric Identifier already exists, <141> found multiple times

OIPE

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 PATENT APPLICATION: US/09/990,080

DATE: 11/28/2001  
 TIME: 12:09:55

Input Set : A:\018258seqList.app  
 Output Set: N:\CRF3\11212001\I990080.raw

**Does Not Comply  
 Corrected Diskette Needed**

3 <110> APPLICANT: Morin, Gregg B.  
 4 Geron Corporation  
 6 <120> TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants  
 8 <130> FILE REFERENCE: 018/258c  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/990,080  
 C--> 11 <141> CURRENT FILING DATE: 2001-11-21  
 W--> 13 <140> CURRENT APPLICATION NUMBER: US 09/128,354  
 C--> 14 <141> CURRENT FILING DATE: 1998-08-03  
 16 <150> PRIOR APPLICATION NUMBER: US 09/052,864  
 17 <151> PRIOR FILING DATE: 1998-03-31  
 19 <160> NUMBER OF SEQ ID NOS: 21  
 21 <170> SOFTWARE: PatentIn Ver. 2.0

#### ERRORED SEQUENCES

343 <210> SEQ ID NO: 2  
 344 <211> LENGTH: 1132  
 345 <212> TYPE: PRT  
 346 <213> ORGANISM: Homo sapiens  
 348 <400> SEQUENCE: 2  
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 350 1 5 10 15  
 352 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
 353 20 25 30  
 355 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
 356 35 40 45  
 358 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 359 50 55 60  
 361 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu  
 362 65 70 75 80  
 364 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val  
 365 85 90 95  
 367 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro  
 368 100 105 110  
 370 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr  
 371 115 120 125  
 373 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg Arg Val  
 374 130 135 140  
 376 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val  
 377 145 150 155 160  
 379 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr  
 380 165 170 175  
 382 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly  
 383 180 185 190  
 385 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg  
 386 195 200 205



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388 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
389      210      215      220
391 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
392 225      230      235      240
394 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
395      245      250      255
397 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
398      260      265      270
400 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
401      275      280      285
403 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
404      290      295      300
406 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
407 305      310      315      320
409 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
410      325      330      335
412 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
413      340      345      350
415 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
416      355      360      365
418 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
419      370      375      380
421 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
422 385      390      395      400
424 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
425      405      410      415
427 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
428      420      425      430
430 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
431      435      440      445
433 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
434      450      455      460
436 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
437 465      470      475      480
439 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
440      485      490      495
442 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
443      500      505      510
445 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
446      515      520      525
448 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
449      530      535      540
451 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
452 545      550      555      560
454 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
455      565      570      575
457 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
458      580      585      590
460 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln

```

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461          595          600          605
463 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
464          610          615          620
466 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
467 625          630          635          640
469 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
470          645          650          655
472 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
473          660          665          670
475 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
476          675          680          685
478 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
479          690          695          700
481 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
482 705          710          715          720
484 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
485          725          730          735
487 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
488          740          745          750
490 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
491          755          760          765
493 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
494          770          775          780
496 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
497 785          790          795          800
499 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
500          805          810          815
502 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
503          820          825          830
505 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
506          835          840          845
508 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
509          850          855          860
511 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
512 865          870          875          880
514 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
515          885          890          895
517 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
518          900          905          910
520 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
521          915          920          925
523 Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
524          930          935          940
526 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
527 945          950          955          960
529 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
530          965          970          975
532 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
533          980          985          990

```

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Input Set : A:\018258seqList.app

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535 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Gln  
 536 995 1000 1005  
 538 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln  
 539 1010 1015 1020  
 541 Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala  
 E--> 542 (025) 1030 1035 1040  
 changed to 544 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu  
 1025 545 1045 1050 1055  
 547 Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp  
 548 1060 1065 1070  
 550 Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr  
 551 1075 1080 1085  
 553 Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser  
 554 1090 1095 1100  
 556 Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn  
 E--> 557 (105) 1110 1115 1120  
 559 Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp  
 560 1125 1130

Numbering  
 misaligned

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/990,080

DATE: 11/28/2001

TIME: 12:09:56

Input Set : A:\018258seqList.app

Output Set: N:\CRF3\11212001\I990080.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:13 M:280 W: Numeric Identifier already exists, <140> found multiple times  
L:13 M:281 W: Numeric Fields not Ordered, <140> not ordered!  
L:13 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:14 M:280 W: Numeric Identifier already exists, <141> found multiple times  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:542 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2  
M:332 Repeated in SeqNo=2